

CLAIMS:

1. A method of detecting an immune system cell, comprising:
contacting a sample comprising cells with a polynucleotide specific for TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), or TMD0890 (XM_060959) of claim 28, under conditions effective for said polynucleotide to hybridize specifically to said gene, and detecting specific hybridization.
2. A method of claim 1, wherein said detecting is performed by:
Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization.
3. A method of detecting an immune system cell, comprising:
contacting a sample comprising cells with a binding partner specific for a polypeptide coded for by TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), or TMD0890 (XM_060959) of claim 28, under conditions effective for said binding partner bind specifically to said polypeptide, and detecting specific binding.
4. A method of claim 3, wherein said detecting is performed by:
immunocytochemistry, immunoprecipitation, or Western blot.
5. A method of delivering an agent to an immune cell, comprising:
contacting an immune cell with an agent coupled to binding partner specific for a polypeptide coded for by TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), or TMD0890 (XM_060959) of claim 28, whereby said agent is delivered to said cell.
6. A method of claim 5, wherein the agent is a therapeutic agent or an imaging agent.

7. A method of claim 5, wherein the agent is cytotoxic.

8. A method of claim 5, wherein the binding partner is an antibody.

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9. A method of modulating the maturation of an immune system cell, comprising:

contacting said cell with an agent effective to modulate a gene, or polypeptide encoded thereby, selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28, whereby the maturation of an immune cell is modulated.

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10. A method of modulating interactions between lymphoid and non-lymphoid immune system cells, comprising:

contacting said cells with an agent effective to modulate a gene, or polypeptide encoded thereby, selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28, whereby the interaction is modulated.

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11. A method of expressing a heterologous polynucleotide in immune system cells, comprising:

expressing a nucleic acid construct in immune system cells, said construct comprising a promoter sequence operably linked to said heterologous polynucleotide, wherein said promoter sequence is selected from SEQ ID NOS 5, 10, 11, 16-19, 29-32, 37-39, 44-46, 51-54, and 59-62.

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12. A method of treating an immune system disease, comprising:

administering to a subject in need thereof a therapeutic agent which is effective for regulating expression of a gene, or polypeptide encoded thereby, selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025

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(XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28.

13. A method of claim 12, wherein said agent is an antibody or an antisense which is effective to inhibit translation of said gene.

14. A method of diagnosing an immune disease associated with abnormal gene expression, or determining a subject's susceptibility to such disease, comprising:

assessing the expression of a gene, or polypeptide encoded thereby, selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28 in a tissue sample comprising immune system cells.

15. A method of claim 14, wherein assessing is:

measuring expression levels of said gene, determining the genomic structure of said gene, determining the mRNA structure of transcripts from said gene, or measuring the expression levels of polypeptide coded for by said gene.

16. A method of claim 14, wherein said assessing detecting is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization, and

using a polynucleotide probe having a sequence selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28, or a polynucleotide probe having 95% sequence identity or more to a sequence set forth in SEQ ID NOS 1, 6, 12, 20, 25, 33, 40, 47, or 55, effective specific fragments thereof, or complements thereto.

17. A method of assessing a therapeutic or preventative intervention in a subject having an

immune system disease, comprising,

determining the expression levels of a gene, or polypeptide encoded thereby, selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28 in a tissue sample comprising immune system cells.

18. A method of claim 17, further comprising assessing the expression levels of a plurality of said genes or polypeptides.

19. A method for identifying an agent that modulates the expression of a gene or polypeptide in the immune system gene complex, comprising,

contacting an immune system cell with a test agent under conditions effective for said test agent to modulate the expression of a gene selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28, or the biological activity of a polypeptide encoded thereby, in said immune system cell, and

determining whether said test agent modulates said gene or polypeptide.

20. A method of claim 19, wherein said agent is an antisense polynucleotide which is effective to inhibit translation of said gene or an antibody specific for said polypeptide.

21. A method of detecting polymorphisms in a gene in the immune system gene complex, comprising: comparing the structure of:

genomic DNA or RNA or cDNA or a polypeptide comprising all or part of a gene selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) of claim 28 with the structure of SEQ ID NOS 1, 6, 12, 20, 25, 33, 40, 47, or 55.

22. A method of claim 20, wherein said polymorphism is a nucleotide deletion, substitution, inversion, or transposition.

5 23. A method of identifying a genetic basis for an immune disease or disease-susceptibility, comprising:

determining the association of an immune disease or disease-susceptibility with a nucleotide sequence present in a genome comprising the gene complex of claim 28.

10 24. A method of claim 23, wherein determining is performed by producing a human-linkage map of said complex.

25. A method of claim 23, wherein determining is performed by comparing the nucleotide sequences between normal subjects and subjects having an immune system disease.

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26. A non-human, transgenic mammal, or a cell thereof, whose genome comprises a functional disruption of a gene selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888

20 (XM_060957), and TMD0890 (XM_060959) of claim 28, or a mouse homolog thereof, and which has a defect in immune system function.

27. A method of selecting a gene predominantly expressed in immune system cells from a database comprising polynucleotide sequences for genes, comprising:

displaying, in a computer-readable medium, a polynucleotide sequence or polypeptide sequence for a gene selected from TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890

5 (XM_060959), or complements to the polynucleotides sequence,

wherein said displayed sequences have been retrieved from said database upon selection by a user.

28. A composition consisting essentially of the 1q22 immune gene complex, comprising
10 TMD0024 (XM_060945), TMD1779 (XM_060946), TMD0884 (XM_060947), TMD0025 (XM_060948), TMD1780 (XM_089422), TMD1781 (XM_089421), TMD0304 (XM_060956), TMD0888 (XM_060957), and TMD0890 (XM_060959) genes, or a fragment thereof comprising at least two said genes.

15 29. A composition of claim 28, wherein said complex consists essentially of the chromosome region between STS markers SHGC-81033 and SHGC-145403, or a fragment thereof comprising at least two said genes.

30. A composition of claim 28, wherein said complex consists essentially of the
20 chromosome region between STS markers SHGC-81033 and D1S3249, G15944, GDB:191077, or GDB:196442, or a fragment thereof comprising at least two said genes.

31. A composition of claim 28, wherein said complex consists essentially of the
25 chromosome region between STS markers RH118729 and D1S2577 or SHGC-145403, or a fragment thereof comprising at least two said genes.

32. A method of detecting an immune system cell, comprising:
contacting a sample comprising cells with a polynucleotide specific for a XM_062147 (SEQ ID NO 63) or XM_061676 (SEQ ID NO 69) of claim 59 under conditions effective for
30 said polynucleotide to hybridize specifically to said gene, and detecting specific hybridization.

33. A method of claim 32, wherein said detecting is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization.

5 34. A method of detecting an immune system cell, comprising:

contacting a sample comprising cells with a binding partner specific for a polypeptide coded for XM_062147 (SEQ ID NO 64) or XM_061676 (SEQ ID NO 70) of claim 59 under conditions effective for said binding partner bind specifically to said polypeptide, and detecting specific binding.

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35. A method of claim 34, wherein said detecting is performed by:

immunocytochemistry, immunoprecipitation, or Western blot.

36. A method of delivering an agent to an immune cell, comprising:

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contacting an immune cell with an agent coupled to binding partner specific for XM_062147 (SEQ ID NO 64) or XM_061676 (SEQ ID NO 70) of claim 59, whereby said agent is delivered to said cell.

37. A method of claim 36, wherein the agent is a therapeutic agent or an imaging agent.

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38. A method of claim 36, wherein the agent is cytotoxic.

39. A method of claim 36, wherein the binding partner is an antibody.

25 40. A method of modulating the maturation of an immune system cell, comprising:

contacting said cell with an agent effective to modulate a gene, or polypeptide encoded thereby, selected from XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59, whereby the maturation of an immune cell is modulated.

30 41. A method of modulating interactions between lymphoid and non-lymphoid immune system cells, comprising:

contacting said cells with an agent effective to modulate a gene, or polypeptide encoded thereby, selected from XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59, whereby the interaction is modulated.

- 5 42. A method of expressing a heterologous polynucleotide in immune system cells, comprising:

expressing a nucleic acid construct in immune system cells, said construct comprising a promoter sequence operably linked to said heterologous polynucleotide, wherein said promoter sequence is SEQ ID NOS 65, 66, 72, 73, 74, or 75.

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43. A method of treating an immune system disease, comprising:

administering to a subject in need thereof a therapeutic agent which is effective for regulating expression of a gene, or polypeptide encoded thereby, selected from XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59.

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44. A method of claim 43, wherein said agent is an antibody or an antisense which is effective to inhibit translation of said gene.

- 20 45. A method of diagnosing an immune disease associated with abnormal gene expression, or determining a subject's susceptibility to such disease, comprising:

assessing the expression of a gene, or polypeptide encoded thereby, selected from XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59 in a tissue sample comprising immune system cells.

- 25 46. A method of claim 45, wherein assessing is:

measuring expression levels of said gene, determining the genomic structure of said gene, determining the mRNA structure of transcripts from said gene, or measuring the expression levels of polypeptide coded for by said gene.

- 30 47. A method of claim 45, wherein said assessing detecting is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR,

RACE PCR, or *in situ* hybridization, and

using a polynucleotide probe having a sequence selected from SEQ ID NOS 67, 68, 76, and 77.

5 48. A method of assessing a therapeutic or preventative intervention in a subject having an immune system disease, comprising,

determining the expression levels of a gene, or polypeptide encoded thereby, selected from XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59 in a tissue sample comprising immune system cells.

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49. A method of claim 48, further comprising assessing the expression levels of a plurality of said genes or polypeptides.

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50. A method for identifying an agent that modulates the expression of a gene or polypeptide in the immune system gene complex, comprising,

contacting an immune system cell with a test agent under conditions effective for said test agent to modulate the expression of XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59, or a polypeptide encoded thereby, in said immune system cell, and

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determining whether said test agent modulates said gene.

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51. A method of claim 50, wherein said agent is an antisense polynucleotide to a target polynucleotide sequence selected from SEQ ID NOS 63 or 69 and which is effective to inhibit translation of said gene.

52. A method of detecting polymorphisms in a gene in the immune system gene complex, comprising:

comparing the structure of: genomic DNA or RNA or cDNA comprising all or part of an allele of XM_062147 or XM_061676 with SEQ ID NOS 63 or 69 of claim 59.

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53. A method of claim 52, wherein said polymorphism is a nucleotide deletion, substitution,

inversion, or transposition.

54. A non-human, transgenic mammal whose genome comprises a functional disruption of a gene represented by XM_062147 (SEQ ID NO 63) or XM_061676 (SEQ ID NO 69) of claim 59, and which has a defect in immune system function.

55. A mammalian immune system cell whose genome comprises a functional disruption of a gene represented by XM_062147 (SEQ ID NO 63) or XM_061676 (SEQ ID NO 69) of claim 59, and which has a defect in immune system function.

56. A mammalian cell of claim 55, wherein said cell is a mouse cell.

57. A non-human, transgenic mammal, or a cell thereof, comprising a gene operatively linked to an expression control sequence effective to express said gene in immune system, wherein said sequence is SEQ ID NOS 65, 66, 71, 72, 73, 74, or 75.

58. A method of selecting a gene predominantly expressed in immune system cells from a database comprising polynucleotide sequences for genes, comprising:

displaying, in a computer-readable medium, a polynucleotide sequence or polypeptide sequence for XM_062147 (SEQ ID NO 63 or 64) or XM_061676 (SEQ ID NO 69 or 70) of claim 59, or complements to the polynucleotides sequence,

wherein said displayed sequences have been retrieved from said database upon selection by a user.

59. A composition comprising:

bone marrow specific genes consisting essentially of XM_062147 (SEQ ID NO 63 or 64) and XM_061676 (SEQ ID NO 69 or 70), or polypeptides thereof.

60. A method of detecting a kidney cell, comprising:

contacting a sample comprising cells with a polynucleotide specific for a polynucleotide, or a naturally-occurring polymorphisms thereof, of claim 81 under conditions effective for said polynucleotide to hybridize specifically to said gene, and

detecting specific hybridization.

61. A method of claim 60, wherein said detecting is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR,

5 RACE PCR, or *in situ* hybridization.

62. A method of detecting an kidney cell, comprising:

contacting a sample comprising cells with a binding partner specific for a polypeptide
coded for by a polynucleotide of claim 81, or a naturally-occurring polymorphism thereof,
10 under conditions effective for said binding partner bind specifically to said polypeptide, and
detecting specific binding.

63. A method of claim 62, wherein said detecting is performed by: immunocytochemistry,
immunoprecipitation, or Western blot.

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64. A method of delivering an agent to a kidney cell, comprising:

contacting a kidney cell with an agent coupled to binding partner specific for
polypeptide coded for by a polynucleotide of claim 81, or a naturally-occurring
polymorphism thereof, whereby said agent is delivered to said cell.

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65. A method of claim 64, wherein the agent is a therapeutic agent, a cytotoxic agent, or an
imaging agent.

66. A method of claim 64, wherein the binding partner is an antibody.

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67. A method of modulating a kidney cell, comprising:

contacting said cell with an agent effective to modulate a polynucleotide, or
polypeptide encoded thereby, or a naturally-occurring polymorphism thereof, of claim 81,
whereby the kidney cell is modulated.

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68. A method of assessing kidney function, comprising:

detecting a polypeptide coded for by a polynucleotide of claim 81, or a naturally-occurring polymorphism thereof, or fragments thereof, in a body fluid, whereby the amount of said polypeptide in said fluid is a measure of kidney function.

5 69. A method of claim 68, wherein said detecting is performed using an antibody which is specific for said polypeptide.

70. A method of claim 69, wherein said detecting is performed by RIA, ELISA, or Western blot.

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71. A method of expressing a heterologous polynucleotide in kidney cells, comprising:
expressing a nucleic acid construct in kidney cells, said construct comprising a promoter sequence operably linked to said heterologous polynucleotide, wherein said promoter sequence is selected from SEQ ID NOS. 106, 109, 110, 113, 114, 117, 118, 121,
15 124, 125, 128-130, 133, 134, 137, 140, 141, 144, 147, 148, and 151.

72. A method of diagnosing a kidney disease associated with abnormal gene expression, or determining a subject's susceptibility to such disease, comprising:

20 assessing the expression of a polynucleotide of claim 81, or a polypeptide encoded thereby, or naturally-occurring polymorphisms thereof, in a tissue sample comprising kidney cells.

73. A method of claim 72, wherein assessing is:

25 measuring expression levels of said gene, determining the genomic structure of said gene, determining the mRNA structure of transcripts from said gene, or measuring the expression levels of polypeptide coded for by said gene.

74. A method of assessing a therapeutic or preventative intervention in a subject having a kidney disease, comprising,

30 determining the expression levels of a polynucleotide of claim 81, a naturally-occurring polymorphism thereof, or polypeptide encoded thereby, in a tissue sample

comprising kidney cells.

75. A method of claim 74, further comprising assessing the expression levels of a plurality of said genes or polypeptides.

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76. A method for identifying an agent that modulates the expression of a polynucleotide or polypeptide selectively expressed in kidney cells, comprising,

contacting an kidney cell with a test agent under conditions effective for said test agent to modulate the expression of a polynucleotide of claim 81, or a naturally-occurring polymorphism thereof, or the biological activity of a polypeptide encoded thereby, in said kidney cell, and

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determining whether said test agent modulates said gene or polypeptide.

77. A non-human, transgenic mammal whose genome comprises a functional disruption of a gene represented by a polynucleotide of claim 81, or a homolog thereof, and which has a defect in kidney function.

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78. A mammalian kidney cell whose genome comprises a functional disruption of a gene represented by a polynucleotide of claim 81, or a homolog thereof, and which has a defect in kidney function.

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79. A mammalian cell of claim 78, wherein said cell is a mouse cell.

80. A method of selecting a gene predominantly expressed in kidney cells from a database comprising polynucleotide sequences for genes, comprising:

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displaying, in a computer-readable medium, a polynucleotide sequence, or a polypeptide encoded thereby, of claim 81, or complements to the polynucleotides sequence, wherein said displayed sequences have been retrieved from said database upon selection by a user.

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81. A composition comprising two or more of the following polynucleotides expressed selectively in kidney:

TMD0049 (XM_057351), TMD0190 (XM_087157), TMD0242 (XM_088369), TMD0335 (XM_089960), TMD0371, TMD0374, TMD0469 (XM_038736), TMD0719 (XM_059548), TMD0731 (XM_059703), TMD0785 (XM_060310), TMD0841 (XM_060623), TMD1114 (NM_019841), and/or TMD 1148 (XM_087108).

82. A method of detecting a pancreas cell, comprising:
contacting a sample comprising cells with a polynucleotide specific for TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, of claim 113 under conditions effective for said polynucleotide to hybridize specifically to said gene, and detecting specific hybridization.

83. A method of claim 82, wherein said detecting is performed by:
Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization.

84. A method of detecting a pancreas cell, comprising:
contacting a sample comprising cells with a binding partner specific for a polypeptide coded for by TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, of claim 113 under conditions effective for said binding partner bind specifically to said polypeptide, and, detecting specific binding.

85. A method of claim 84, wherein said detecting is performed by:
immunocytochemistry, immunoprecipitation, or Western blot.

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86. A method of delivering an agent to a pancreas cell, comprising:
contacting a pancreas cell with an agent coupled to binding partner specific for

TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, of claim 113, whereby said agent is delivered to said cell.

87. A method of claim 86, wherein the agent is a therapeutic agent or an imaging agent.

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88. A method of claim 86, wherein the agent is cytotoxic.

89. A method of claim 86, wherein the binding partner is an antibody.

10 90. A method of modulating a pancreas cell, comprising:

contacting said cell with an agent effective to modulate TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, or the biological activity of a polypeptide encoded thereby, of claim 113, whereby the pancreas cell is modulated.

15 91. A method of assessing pancreas function, comprising:

detecting a polypeptide coded for TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, or fragments thereof, in a body fluid, whereby the amount of said polypeptide in said fluid is a measure of pancreas function.

20 92. A method of claim 91, wherein said detecting is performed using an antibody which is specific for said polypeptide.

93. A method of claim 91, wherein said detecting is performed by RIA, ELISA, or Western blot.

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94. A method of expressing a heterologous polynucleotide in pancreas cells, comprising:

expressing a nucleic acid construct in pancreas cells, said construct comprising a promoter sequence operably linked to said heterologous polynucleotide, wherein said promoter sequence is SEQ ID NOS 156-161, 166, 179, or 180.

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95. A method of diagnosing a pancreas disease associated with abnormal gene expression,

or determining a subject's susceptibility to such disease, comprising:

assessing the expression of TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, or polypeptide encoded thereby, of claim 113 in a tissue sample comprising pancreas cells.

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96. A method of claim 95, wherein assessing is:

measuring expression levels of said gene, determining the genomic structure of said gene, determining the mRNA structure of transcripts from said gene, or measuring the expression levels of polypeptide coded for by said gene.

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97. A method of claim 95, wherein said assessing is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization, and

using a polynucleotide probe having a sequence selected from SEQ ID NOS 154, 155, 164, 165, 169, 170, 173, 174, 177, 178, or a complement thereto.

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98. A method of assessing a therapeutic or preventative intervention in a subject having a pancreas disease, comprising,

determining the expression levels of TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, or a polypeptide encoded thereby, of claim 113 in a tissue sample comprising pancreas cells.

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99. A method of claim 98, further comprising assessing the expression levels of a plurality of said genes or polypeptides.

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100. A method for identifying an agent that modulates the expression of TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, or the biological activity of a polypeptide encoded thereby, comprising,

contacting a pancreas cell with a test agent under conditions effective for said test agent to modulate the expression of TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785 of claim 113, or the biological activity of a polypeptide encoded thereby, in said

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pancreas cell, and

determining whether said test agent modulates said gene or polypeptide.

101. A method of claim 100, wherein said agent is an antisense polynucleotide to a target
5 polynucleotide sequence selected from SEQ ID NO 152, 162, 167, 171, or 175 and which is effective to inhibit translation of said gene.

102. A method of detecting polymorphisms in TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, comprising,

10 comparing the structure of: genomic DNA or RNA or cDNA comprising all or part of an allele of TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785, with SEQ ID NOS 152, 153, 162, 163, 167, 168, 171, 172, 175, or 176 of claim 113.

103. A method of claim 102, wherein said polymorphism is a nucleotide deletion,
15 substitution, inversion, or transposition.

104. A method of identifying a pancreatic disease or pancreatic disease-susceptibility, comprising:

20 determining the association of a pancreatic disease or pancreatic disease-susceptibility with a nucleotide sequence present within the pancreatic gene complex of claim 113.

105. A method of claim 104, wherein the pancreatic gene complex is from LOC160025-LOC119954.

106. A method of claim 104, wherein determining is performed by producing a human-
25 linkage map of said complex.

107. A method of claim 104, wherein determining is performed by comparing the nucleotide sequences between normal subjects and subjects having a pancreas disorder.

30 108. A non-human, transgenic mammal whose genome comprises a functional disruption of a gene represented by TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785

of claim 113, and which has a defect in pancreas function.

109. A mammalian pancreas cell whose genome comprises a functional disruption of a gene represented by TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785 of claim
5 113, and which has a defect in pancreas function.

110. A mammalian cell of claim 109, wherein said cell is a mouse cell.

111. A pancreas cell, comprising a gene operatively linked to an expression control sequence
10 effective to express said gene in pancreas, wherein said sequence is SEQ ID NOS 156-161, 179, or 180.

112. A method of selecting a gene predominantly expressed in pancreas cells from a database comprising polynucleotide sequences for genes, comprising:

15 displaying, in a computer-readable medium, a polynucleotide sequence or polypeptide sequence for TMD0986, XM_061780, XM_061781, XM_061784, or XM_061785 of claim 113, or complements to the polynucleotides sequence,
wherein said displayed sequences have been retrieved from said database upon selection by a user.

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113. A composition comprising: a pancreas specific gene consisting essentially of TMD0986, XM_061780, XM_061781, XM_061784, and/or XM_061785, or a polypeptide encoded thereby.

25 114. An isolated polynucleotide comprising a polynucleotide sequence which codes without interruption for a human TMD0986 having an amino acid sequence set forth in SEQ ID NO 153, or a complement thereto.

115. An isolated polynucleotide comprising,
30 a human TMD0986 polynucleotide sequence having 90% or more nucleotide sequence identity to the polynucleotide sequence set forth in SEQ ID NO 152 along its entire

length, which codes without interruption for human TMD0986, or a complement thereto, and which has G-protein coupling activity.

116. An isolated humansTMD0986 polypeptide comprising the amino acid sequence of a human TMD0986 as set forth in SEQ ID NO 153.

117. An isolated human TMD0986 polypeptide consisting essentially of amino acids 1-117 of a human TMD0986 as set forth in SEQ ID NO 153.

118. An isolated polypeptide which is human TMD0986 having 90% or more amino acid sequence identity to the amino acid sequence set forth in SEQ ID NO 153, and which has protein binding activity.

119. An antibody specific for an epitope selected from the polypeptide of claim 117.

120. A method of detecting an retinal cell, comprising:

contacting a sample comprising cells with a polynucleotide specific for NM_013941 (SEQ ID NO 181), or a naturally-occurring polymorphisms thereof, of claim 142 under conditions effective for said polynucleotide to hybridize specifically to said gene, and detecting specific hybridization.

121. A method of claim 120, wherein said detecting is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization.

122. A method of detecting an retinal cell, comprising:

contacting a sample comprising cells with a binding partner specific for a polypeptide coded for by NM_013941 (SEQ ID NO 182), or a naturally-occurring polymorphism thereof, of claim 142 under conditions effective for said binding partner bind specifically to said polypeptide, and detecting specific binding.

123. A method of claim 122, wherein said detecting is performed by:
immunocytochemistry, immunoprecipitation, or Western blot.

124. A method of delivering an agent to a retinal cell, comprising:

5 contacting a retinal cell with an agent coupled to binding partner specific for by
NM_013941 (SEQ ID NO 182), or naturally-occurring polymorphism thereof, of claim 142,
whereby said agent is delivered to said cell.

125. A method of claim 124, wherein the agent is a therapeutic agent or an imaging agent.

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126. A method of claim 124, wherein the agent is cytotoxic.

127. A method of claim 124, wherein the binding partner is an antibody.

15 128. A method of modulating a retinal cell, comprising:

 contacting said cell with an agent effective to modulate NM_013941 (SEQ ID NO
181 or 182), or the biological activity of a polypeptide encoded thereby, of claim 142,
whereby the retinal cell is modulated.

20 129. A method of diagnosing a retinal disease associated with abnormal gene expression, or
determining a subject's susceptibility to such disease, comprising:

 assessing the expression of NM_013941, a polymorphism thereof, or polypeptide
encoded thereby, of claim 142 in a tissue sample comprising retinal cells.

25 130. A method of claim 129, wherein assessing is:

 measuring expression levels of said gene, determining the genomic structure of said
gene, determining the mRNA structure of transcripts from said gene, or measuring the
expression levels of polypeptide coded for by said gene.

30 131. A method of claim 129, wherein said assessing detecting is performed by:

 Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR,

RACE PCR, or *in situ* hybridization, and

using a polynucleotide probe having a sequence selected from SEQ ID NOS 183 or 184, or a complement thereto.

- 5 132. A method of assessing a therapeutic or preventative intervention in a subject having an retinal disease, comprising,
- determining the expression levels of NM_013941, a polymorphism thereof, or polypeptide encoded thereby, of claim 142 in a tissue sample comprising retinal cells.
133. A method of claim 132, further comprising assessing the expression levels of a plurality
- 10 of said genes or polypeptides.
134. A method for identifying an agent that modulates the expression of NM_013941 or the biological activity of a polypeptide encoded thereby, comprising,
- contacting an retinal cell with a test agent under conditions effective for said test
- 15 agent to modulate the expression of NM_013941 or a polymorphism thereof, of claim 142, or the biological activity of a polypeptide encoded thereby, in said retinal cell, and
- determining whether said test agent modulates said gene or polypeptide.
135. A method of claim 134, wherein said agent is an antisense polynucleotide to a target
- 20 polynucleotide sequence selected from SEQ ID NO 181 and which is effective to inhibit translation of said gene.
136. A method of detecting polymorphisms in NM_013941, comprising:
- comparing the structure of: genomic DNA or RNA or cDNA comprising all or part
- 25 of an allele of NM_013941, with SEQ ID NOS 181 or 182 of claim 142.
137. A method of claim 136, wherein said polymorphism is a nucleotide deletion, substitution, inversion, or transposition.
- 30 138. A non-human, transgenic mammal whose genome comprises a functional disruption of a gene represented by NM_013941 (SEQ ID NO 181) of claim 142, and which has a defect in

retinal function.

139. A mammalian retinal cell whose genome comprises a functional disruption of a gene represented by NM_013941 (SEQ ID NO 181) of claim 142, and which has a defect in retinal
5 function.

140. A mammalian cell of claim 139, wherein said cell is a mouse cell.

141. A method of selecting a gene predominantly expressed in retinal cells from a database
10 comprising polynucleotide sequences for genes, comprising:
displaying, in a computer-readable medium, a polynucleotide sequence or polypeptide
sequence for NM_013941 (SEQ ID NO 181 or 182) of claim 142, or complements to the
polynucleotides sequence,
wherein said displayed sequences have been retrieved from said database upon
15 selection by a user.

142. A composition comprising:
a retinal specific gene consisting essentially of NM_013941 (SEQ ID NO 181 or
182), or a polypeptide encoded thereby.

20 143. A method of detecting a spleen cell, comprising:
contacting a sample comprising cells with a polynucleotide specific for TMD1030
(XM_166853) or TMD0621 (XM_166205) of claim 170 under conditions effective for said
polynucleotide to hybridize specifically to said gene, and
25 detecting specific hybridization.

144. A method of claim 143, wherein said detecting is performed by:
Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR,
RACE PCR, or *in situ* hybridization.

30 145. A method of detecting a spleen cell, comprising:
contacting a sample comprising cells with a binding partner specific for a polypeptide

coded for by TMD1030 (XM_166853) or TMD0621 (XM_166205) of claim 170 under conditions effective for said binding partner bind specifically to said polypeptide, and detecting specific binding.

5 146. A method of claim 145, wherein said detecting is performed by:
immunocytochemistry, immunoprecipitation, or Western blot.

147. A method of delivering an agent to a spleen cell, comprising:
contacting a spleen with an agent coupled to binding partner specific for TMD1030
10 (XM_166853) or TMD0621 (XM_166205) of claim 170, whereby said agent is delivered to
said cell.

148. A method of claim 147, wherein the agent is a therapeutic agent or an imaging agent.

15 149. A method of claim 148, wherein the agent is cytotoxic.

150. A method of claim 147, wherein the binding partner is an antibody.

151. A method of modulating a spleen, immune, or reticuloendothelial cell, comprising:
20 contacting said cell with an agent effective to modulate TMD1030 (XM_166853),
TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205), or the
biological activity of a polypeptide encoded thereby, of claim 170, whereby the cell is
modulated.

25 152. A method of assessing spleen function, comprising:
detecting a polypeptide coded for by TMD1030 (XM_166853) or TMD0621
(XM_166205) of claim 170, or fragments thereof, in a body fluid, whereby the amount of
said polypeptide in said fluid is a measure of spleen function.

30 153. A method of claim 152, wherein said detecting is performed using an antibody which is
specific for said polypeptide.

154. A method of claim 152, wherein said detecting is performed by RIA, ELISA, or Western blot.

5 155. A method of expressing a heterologous polynucleotide in spleen cells, comprising:
expressing a nucleic acid construct in spleen cell, said construct comprising a promoter sequence operably linked to said heterologous polynucleotide, wherein said promoter sequence is SEQ ID NO 205-213.

10 156. A method of assessing a therapeutic or preventative intervention in a subject having a spleen or lymphoid disease, comprising,
determining the expression levels of TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205), or a polypeptide encoded thereby, of claim 170 in a tissue sample comprising spleen, lymphoid, or
15 reticuloendothelial cells.

157. A method of claim 156, further comprising assessing the expression levels of a plurality of said genes or polypeptides.

20 158. A method for identifying an agent that modulates the expression of TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205), comprising,
contacting a spleen, lymphoid, or reticuloendothelial cell, with a test agent under conditions effective for said test agent to modulate the expression of TMD1030
25 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205), of claim 170, and
determining whether said test agent modulates said gene.

30 159. A method of claim 158, wherein said agent is an antisense which is effective to inhibit translation of said gene.

160. A method for identifying an agent that modulates the expression of a polypeptide coded for by TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205), comprising,

contacting a polypeptide coded for by TMD1030 (XM_166853), TMD1029

5 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205) of claim 170, with a test agent under conditions effective for said test agent to modulate said polypeptide, and determining whether said test agent modulates said polypeptide.

161. A method of detecting polymorphisms in comprising, comparing the structure of :

10 genomic DNA or RNA or cDNA comprising all or part of an allele of TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205), with SEQ ID NOS 185, 187, 189, or 191 of claim 170.

162. A method of claim 161, wherein said polymorphism is a nucleotide deletion,

15 substitution, inversion, or transposition.

163. A method of identifying a genetic basis for a spleen, lymphoid, and/or

reticuloendothelial disease or disease-susceptibility, comprising: determining the association of a spleen, lymphoid, and/or reticuloendothelial disease or disease-susceptibility with a

20 nucleotide sequence present in the gene complex of claim 170.

164. A method of claim 163, wherein determining is performed by producing a human-linkage map of said complex.

25 165. A method of claim 163, wherein determining is performed by comparing the nucleotide sequences between normal subjects and subjects having a spleen, lymphoid, and/or reticuloendothelial disease.

166. A non-human, transgenic mammal, or a cell thereof. whose genome comprises a

30 functional disruption of a gene represented by TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205) of claim 170, and

which has a defect in spleen, lymphoid, and/or reticuloendothelial disease function.

167. A mammalian cell of claim 166, wherein said cell is a mouse cell.

5 168. A spleen, lymphoid, and/or reticuloendothelial cell, comprising a gene operatively linked to an expression control sequence effective to express said gene in spleen, lymphoid, and/or reticuloendothelial, wherein said sequence is SEQ ID NO 205-213.

169. A method of selecting a gene predominantly expressed in spleen, lymphoid, and/or
10 reticuloendothelial cells from a database comprising polynucleotide sequences for genes, comprising:

displaying, in a computer-readable medium, a polynucleotide sequence or polypeptide sequence for TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), or TMD0621 (XM_166205) of claim 170, or complements to the
15 polynucleotides sequence, wherein said displayed sequences have been retrieved from said database upon selection by a user.

170. A composition consisting essentially of the 11q12.2 spleen gene complex, comprising
TMD1030 (XM_166853), TMD1029 (XM_166854), TMD1028 (XM_166855), and
20 TMD0621 (XM_166205).

171. A composition of claim 170, wherein said complex consists essentially of the chromosome region between STS markers G62658 and SHGC-154002.

25 172. A method of detecting a pancreas cell, comprising:
contacting a sample comprising cells with a polynucleotide specific TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127 of claim 199
30 under conditions effective for said polynucleotide to hybridize specifically to said gene, and detecting specific hybridization.

173. A method of claim 172, wherein said detecting is performed by:

Northern blot analysis, polymerase chain reaction (PCR), reverse transcriptase PCR, RACE PCR, or *in situ* hybridization.

5 174. A method of detecting a pancreas cell, comprising:

contacting a sample comprising cells with a binding partner specific for a polypeptide coded for by TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or
10 TMD1127

of claim 199 under conditions effective for said binding partner bind specifically to said polypeptide, and

detecting specific binding.

15 175. A method of claim 174, wherein said detecting is performed by:

immunocytochemistry, immunoprecipitation, or Western blot.

176. A method of delivering an agent to a pancreas cell, comprising:

contacting a pancreas with an agent coupled to binding partner specific for
20 TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127 of claim 199, whereby said agent is delivered to said cell.

25 177. A method of claim 176, wherein the agent is a therapeutic agent or an imaging agent.

178. A method of claim 176, wherein the agent is cytotoxic.

179. A method of claim 176, wherein the binding partner is an antibody.

30

180. A method of modulating a pancreas, immune, or reticuloendothelial cell, comprising:

contacting said cell with an agent effective to modulate TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127, or the biological activity of a polypeptide encoded thereby, of claim 199, whereby the cell is modulated.

181. A method of assessing pancreas function, comprising:

detecting a polypeptide coded for by TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127 of claim 199, or fragments thereof, in a body fluid, whereby the amount of said polypeptide in said fluid is a measure of pancreas function.

182. A method of claim 181, wherein said detecting is performed using an antibody which is specific for said polypeptide.

183. A method of claim 181, wherein said detecting is performed by RIA, ELISA, or Western blot.

184. A method of expressing a heterologous polynucleotide in pancreas cells, comprising:

expressing a nucleic acid construct in pancreas cell, said construct comprising a promoter sequence operably linked to said heterologous polynucleotide, wherein said promoter sequence is selected SEQ ID NO 258, 261, 262, 265-267, 270-272, 275, 278, 279, 282-284, 287, 290-293, 296, 297, 300, 303, 306, 309-314, 317-320, 323-326, 329, 332-333, 336-338, 341, and 344.

185. A method of assessing a therapeutic or preventative intervention in a subject having a pancreas or lymphoid disease, comprising,

determining the expression levels of TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127, or a polypeptide encoded thereby, of claim 199 in

a tissue sample comprising pancreas, lymphoid, or reticuloendothelial cells.

186. A method of claim 185, further comprising assessing the expression levels of a plurality of said genes or polypeptides.

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187. A method for identifying an agent that modulates the expression of TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127, comprising,

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contacting a pancreas, lymphoid, or reticuloendothelial cell, with a test agent under conditions effective for said test agent to modulate the expression of TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127, of claim 199, and

15

determining whether said test agent modulates said gene.

188. A method of claim 187, wherein said agent is an antisense which is effective to inhibit translation of said gene.

20

189. A method for identifying an agent that modulates the expression of a polypeptide coded for by TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127, comprising,

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contacting a polypeptide coded for by TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127 of claim 199, with a test agent under conditions effective for said test agent to modulate said polypeptide, and

30

determining whether said test agent modulates said polypeptide.

190. A method of claim 189, wherein said test agent is an antibody.

191. A method of detecting polymorphisms in comprising, comparing the structure of :
genomic DNA or RNA or cDNA comprising all or part of an allele of

5 TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290,
TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675,
TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127,
with SEQ ID NOS of Table 23 of claim 199.

10 192. A method of claim 191, wherein said polymorphism is a nucleotide deletion,
substitution, inversion, or transposition.

193. A method of identifying a genetic basis for a pancreas disease or disease-susceptibility,
comprising: determining the association of a pancreas disease or disease-susceptibility with a
15 gene of claim 199.

194. A method of claim 193, wherein determining is performed by producing a human-
linkage map of said gene.

20 195. A method of claim 193, wherein determining is performed by comparing the
nucleotide sequences between normal subjects and subjects having a pancreas disease.

196. A non-human, transgenic mammal, or a cell thereof. whose genome comprises a
functional disruption of a gene represented by TMD0077, TMD0233, TMD0256, TMD0258,
25 TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639,
TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739,
TMD0753, TMD1111, and/or TMD1127, of claim 199, and which has a defect in pancreas,
lymphoid, and/or reticuloendothelial disease function.

30 197. A mammalian cell of claim 196, wherein said cell is a mouse cell.

198. A method of selecting a gene predominantly expressed in pancreas tissue from a

database comprising polynucleotide and amino acid sequences for genes, comprising:

displaying, in a computer-readable medium, a polynucleotide sequence or polypeptide sequence for TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127, of claim 199, or complements to the polynucleotides sequence, wherein said displayed sequences have been retrieved from said database upon selection by a user.

10 199. A composition comprising genes and/or polypeptide which are expressed predominantly in pancreas tissue comprising:

TMD0077, TMD0233, TMD0256, TMD0258, TMD0267, TMD0271, TMD0290, TMD0530, TMD0574, TMD0608, TMD0639, TMD0645, TMD0674, TMD0675, TMD0677, TMD0726, TMD0727, TMD0739, TMD0753, TMD1111, and/or TMD1127.